REMARKS

Applicant thanks the Examiner for her consideration of his April 30, 2007 Response and her withdrawing of the 102(b) rejection over <u>Telang</u>.

The Claim Amendments

Applicant has amended claims 45 and 46 to clarify that the claimed method is a culture-independent one. This amendment is supported in the specification, for example, at page 3, lines 11-12; page 4, line 20; page 13, lines 8-12; page 14, lines 15-26; page 18, lines 16-17 and page 38, lines 3-4). Applicant has also amended claims 45 and 46 to recite a correlation between the abundance of the markers and the abundance of the parameter of interest. This amendment is supported in the specification, for example, at page 24, line 12; page 27, lines 12-14; and Figs. 5, 6, and 7. Applicant has further amended claims 45 and 46 to clarify that one or more nucleic marker sequences can be utilized. This amendment is supported in the specification, for example, at page 15, lines 22-23. Applicant has further amended claims 45 and 46 to improve their form.

Applicant has amended claims 47-49 to recite a correlation between the abundance of the marker and the abundance of the parameter of interest. This amendment is supported in the specification, for example, at page 24, line 12; page 27, lines 12-14; and Figs. 5, 6, and 7.

Applicant has added claim 57 to recite the selection of a nucleic acid marker sequences based on the level of the correlation of their abundance to the abundance of a parameter of interest. This amendment is supported in the specification, for example, at page 27, line 8 to page 28, line 9, and Fig. 6.

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Claim Interpretation

The Examiner asserts that the correlation ("perfect", "high", and "moderate") is not defined. Applicant respectfully traverses.

Page 29, lines 15-17, defines moderate correlation ("r is 0.5 to 0.7"), and high correlation ("r is 0.8 to 0.99"). These are not "possible" or "may be" definitions. They are "is" definitions. The definition of perfect correlation as being r=1 is also not a "may be" definition. Rather, it is a standard definition (see, for example, Van Nostrand's Scientific Encyclopedia. Fifth Edition. 1976, p. 688, copy included).

Finally, applicant has amended the claims to refer to an abundance (a number value). For these reasons, applicant requests that the Examiner reconsider and withdraw her objections to the claims and their terms.

Rejections

35 U.S.C. §102(b) - Anticipation

Claims 45-49 stand rejected under 35 U.S.C. §102(b) as being allegedly anticipated by Goldsteyn-Thomas et al., Applied Environmental Microbiology, 1991, p. 2576 ("Goldsteyn-Thomas"). The Examiner contends that Goldsteyn-Thomas recites a method of identifying an environmental parameter of interest by identifying the presence of a nucleic acid marker sequence by a) providing an environmental sample, b) isolating genomic DNA from the sample, c) assaying the genomic DNA utilizing a plurality of species-specific probes to the nucleic acid marker sequence that shows a correlation for the parameter of interest, and

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d) inferring the presence of the parameter of interest based upon the presence of the nucleic acid marker sequence in the genomic DNA isolated from the sample. Applicant traverses.

Applicant's invention and the methods recited in <u>Goldsteyn-Thomas</u> are totally different. The methods of the claimed invention comprise identifying and using species-specific DNA sequences as molecular indicators, wherein the abundance of these indicators or markers is correlated to the abundance of a parameter of interest. More particularly, amended claims 45 and 46, and the claims that depend therefrom, are directed to methods of determining the abundance of environmental parameters of interest using probes for at least one nucleic acid marker sequence whose abundance correlates to the abundance of the parameter. In contrast, the method recited in <u>Goldsteyn-Thomas</u> utilizes PCR to detect the presence of the listeriolysin O gene, a gene specific to L. monocytogenes, from genomic DNA isolated from samples. There is no recitation that the detection of the listeriolysin O gene in <u>Goldsteyn-Thomas</u> correlates in anyway to the abundance of a parameter of interest.

In addition, the method employed in <u>Goldsteyn-Thomas</u> is different from the claimed invention in another fundamental aspect. As amended, claims 45 and 46 recite, "A <u>culture-independent</u> method of determining the abundance of an environmental parameter". In <u>Goldsteyn-Thomas</u>, the milk or meat sample is cultured before the PCR assay (see, e.g., p. 2576, Materials and Methods, second paragraph). For that reason alone, <u>Goldsteyn-Thomas</u> does not anticipate the invention of the amended claims.

The "cultured" vs. "not cultured" distinction between the claimed invention and the method of <u>Goldsteyn-Thomas</u> is an important difference. Culturing a sample before it is assayed will result in some microorganisms propagating more readily than others. This changes the relative concentration of the organisms in the sample. Further, far fewer than 1% of

microbes can propagate under laboratory conditions (see specification, page 4, line 20). This results in many of the species within the sample being lost during culturing. Therefore, assaying the genomic DNA isolated from a sample without culturing, as taught by applicant, produces a more accurate representation of the original sample, and, thus, a more accurate assay of the abundance of the environment and parameter than the cultured-based method of <u>Goldsteyn-</u>Thomas (if it had even tried to measure or correlate abundances which it did not).

For the above reasons, applicant requests that Examiner reconsider and withdraw the 102(b) rejection.

35 U.S.C. §103(a) - Obviousness

Claims 45-50 stand rejected under 35 U.S.C. §103(a) as being allegedly unpatentable over Leu et al., Anaerobe, 1998, pp. 165-174 ("Leu"). The Examiner contends that Leu recites a method of identifying the presence of an environmental parameter of interest by identifying the presence of a nucleic acid marker sequence by: a) providing an environmental sample, b) isolating genomic DNA from the sample, c) assaying the genomic DNA utilizing a plurality of species-specific probes to the nucleic acid marker sequence that shows a correlation for the parameter of interest, and d) inferring the presence of the parameter of interest based upon the presence of the nucleic acid marker sequence in the genomic DNA isolated from the sample. The Examiner further contends that, although Leu does not specifically recite using species-specific primers or probes in the analysis of oil field samples, Leu suggests using the cloned sulfate-reducing bacteria (SRB) sequences to obtain species-specific probes to identify individual SRBs, and that it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to have used species-specific primers. Applicant traverses.

The Examiner's contention that <u>Leu</u> recites a method of identifying the presence of hydrogen sulfide in oil fields by identifying the presence of the 16S rDNA of SRBs is mistaken. The methods recited in <u>Leu</u> identify thermophilic SRBs in samples taken from oil reservoirs. They do <u>not</u> identify reservoirs with hydrogen sulfide. In fact, according to <u>Leu</u>, SRB-related sequences are present in all oil field samples (e.g., see Introduction, p. 166, third paragraph). <u>Leu</u> also recites that SRBs appear to be common and widely distributed over oil field environments, presumably even in environments that lack hydrogen sulfide (see page 170, fourth paragraph). Therefore, according to <u>Leu</u>, the presence of the SRBs is <u>completely uncorrelated</u> with the presence of hydrogen sulfide. As such, <u>Leu</u> does not suggest or allow making inferences regarding the abundance of hydrogen sulfide in oil fields based on the presence of SRBs.

Finally, <u>Leu</u> recites detecting, but not determining, the abundance of a nucleic acid marker sequence within the genomic DNA collected from the sample. In contrast, the claimed invention involves correlating the abundance of a nucleic acid marker sequence with the abundance of an environmental parameter (see, e.g., page 24, line 12, page 27, lines 12-14, and Figs. 5,6,7 in the specification).

For the above reasons, applicant requests that the Examiner reconsider and withdraw the 103(a) rejection.

CONCLUSION

Applicant requests consideration of the amended claims in view of the foregoing remarks and allowance of those claims.

Should the Examiner feel that a telephone conference with applicant's representative would be helpful, she is invited to telephone the undersigned at any time.

Respectfully submitted,

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